

D. Bugaiko

1653

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**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/981,998**

DATE: 08/03/1999
TIME: 15:47:46

INPUT SET: S32762.raw

#11

This Raw Listing contains the General Information Section and up to the first 5 pages.

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SEQUENCE LISTING

**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/981,998**DATE: 08/03/1999
TIME: 15:47:46**INPUT SET: S32762.raw**

47 (viii) ATTORNEY/AGENT INFORMATION:
48 (A) NAME: MUETING, ANN M.
49 (B) REGISTRATION NUMBER: 33,977
50 (C) REFERENCE/DOCKET NUMBER: 232.00010120
51

52 (ix) TELECOMMUNICATION INFORMATION:
53 (A) TELEPHONE: 612-305-1217
54 (B) TELEFAX: 612-305-1228
55

56 (2) INFORMATION FOR SEQ ID NO:1:

57 (i) SEQUENCE CHARACTERISTICS:
58 (A) LENGTH: 516 base pairs
59 (B) TYPE: nucleic acid
60 (C) STRANDEDNESS: both
61 (D) TOPOLOGY: both
62

63 (ii) MOLECULE TYPE: DNA (genomic)
64

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66

67 TTGGTAGCAA CGGAAACGGC GGCGGCGCGT TTCGGCCCGG CTCCCGGCCG CTCCTTGGTC 60
68 TCGGCGGGCC TCCCCGCCCC TTCTCGTCG TCCTTCTCCC CCTCGCCAGC CGGGCGGCC 120
69 CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCG TGCCTCCCCG CCGCGTTCCG 180
70 GCGTCTCCTT GGCGCGCCCG GCTCCCGGT GTCCCCGCCG GGCCTGCGAG CCGGTGTATG 240
71 GGCCCTCAC CATTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC 300
72 AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA 360
73 AGCCCGGGCGG CAGCGGCCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCCT 420
74 CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGCGACC TCCGGGGCG 480
75 GGAGGCCCGG CCTGGGCAGG TGGGTGTCGG CACCCCC 516
76

77 (2) INFORMATION FOR SEQ ID NO:2:
78

79 (i) SEQUENCE CHARACTERISTICS:
80 (A) LENGTH: 4481 base pairs
81 (B) TYPE: nucleic acid
82 (C) STRANDEDNESS: both
83 (D) TOPOLOGY: both
84

85 (ii) MOLECULE TYPE: cDNA
86

87

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100							
101	(ix) FEATURE:						
102	(A) NAME/KEY: CDS						
103	(B) LOCATION: 163..4101						
104							
105							
106	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:						
107							
108	ACCCCCGAGA	AAGCAACCCA	GCGCGCCGCC	CGCTCCTCAC	GTGTCCCTCC	CGGGCCCCGGG	60
109							
110	GCCACCTCAC	GTTCTGCTTC	CGTCTGACCC	CTCCGACTTC	CGGTAAAGAG	TCCCTATCCG	120
111							
112	CACCTCCGCT	CCCACCCGGC	GCCTCGGCGC	GCCCCGCCCTC	CG ATG CGC TCA GCG	Met Arg Ser Ala	174
113							
114				1			
115							
116							
117	GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC	Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe	5	10	15	20	222
118							
121	GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG	Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg	25	30	35	270	
122							
125	CGG AGC GGG CGG GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC	Arg Ser Gly Arg Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser	40	45	50	318	
126							
129	GCC GCC CCT CCC CCG CCC GGC CCC CCT CCC TCC CGG CAG AGC	Ala Ala Pro Pro Pro Gly Pro Gly Pro Pro Ser Arg Gln Ser	55	60	65	366	
130							
133	TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC	Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly	70	75	80	414	
134							
137	GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT	Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Pro	85	90	95	100	462
138							
141	CCC CGC CCC TTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC	Pro Arg Pro Phe Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala	105	110	115	510	
142							
145	CCT CCC GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC	Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser	120	125	130	558	
146							
149	CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC	Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro	135	140	145	606	
150							
152							

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153	CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG	654
154	Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys	
155	150 155 160	
156		
157	CCC CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG	702
158	Pro Gln	
159	165 170 175 180	
160		
161	CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC	750
162	Gln Gln Gln Gln Gln Pro Pro Ala Ala Ala Asn Val Arg	
163	185 190 195	
164		
165	AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG CCT TCG	798
166	Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser	
167	200 205 210	
168		
169	CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC ACG GCT CCC TCC TCG	846
170	Pro Ser Ser Ser Val Ser Ser Ser Ala Thr Ala Pro Ser Ser	
171	215 220 225	
172		
173		
174		
175	GTG GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC AGA GGT	894
176	Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly	
177	230 235 240	
178		
179	CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT GAT GGA	942
180	Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly	
181	245 250 255 260	
182		
183	ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT GTT GGC	990
184	Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val Val Gly	
185	265 270 275	
186		
187	TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA GGA GTT	1038
188	Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val	
189	280 285 290	
190		
191	TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT	1086
192	Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His	
193	295 300 305	
194		
195	GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG	1134
196	Glu Lys Ser Thr Glu Ser Ser Gly Pro Lys Arg Glu Glu Ile Met	
197	310 315 320	
198		
199	GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA	1182
200	Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys	
201	325 330 335 340	
202		
203	GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT	1230
204	Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala	
205	345 350 355	

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206	ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC		1278
207	Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro		
208	360	365	370
209			
210			
211	TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA		1326
212	Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu		
213	375	380	385
214			
215	AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT		1374
216	Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn		
217	390	395	400
218			
219	GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG		1422
220	Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser		
221	405	410	415
222			
223	TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG		1470
224	Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg		
225	425	430	435
226			
227	GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT GCC CAG		1518
228	Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln		
229	440	445	450
230			
231			
232			
233	TAC AAA GCT CGA GTG GCC CTG GAA AAT GAT GAT AGG AGT GAG GAA GAA		1566
234	Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu		
235	455	460	465
236			
237	AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG CAC AGC		1614
238	Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly His Ser		
239	470	475	480
240			
241	ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA AAT AGA		1662
242	Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg		
243	485	490	495
244			
245	GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT ATG GGC		1710
246	Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg Met Gly		
247	505	510	515
248			
249	CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC ACT TCA		1758
250	Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His Thr Ser		
251	520	525	530
252			
253	GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT GGA GGT		1806
254	Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn Gly Gly		
255	535	540	545
256			
257	GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA CCT TCT		1854
258	Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Arg Pro Pro Ser		

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SEQUENCE VERIFICATION REPORT
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Original Text